

### *Amendments to the Drawings*

In Figure 7A (Formal Drawing 7A-1), the following minor changes have been made: 1) the line demarcating the transmembrane region has been shortened such that it extends only over the L at position 72 and no further; 2) the amino acid number designation "77", at the end of the first line of LT-alpha sequence has been changed to "76"; and 3) the "G" at position 197 of Neutrokin-alpha sequence was changed from being white on black to being black on white. Copies of the original drawing, in both its informal and formal form, are attached with these changes marked in red.

The amendment of the length of the line demarcating the transmembrane region brings the drawing into conformity with the description of the transmembrane region as it is defined in the specification in several locations. See for example page 10, lines 20-23 where the transmembrane region is defined as amino acids 47 to 72 of the Neutrokin-alpha polypeptide. Thus, this amendment introduces no new matter and is fully supported by the specification.

The amendment of the amino acid number designation corrects the numbering of the sequence such that it agrees with the numbering of the sequence of Lymphotoxin-alpha given in Gray, *Nature* 312,721-724 (1984). The Gray *et al.* Nature article is cited on page 412, line 15 of the specification in reference to Figure 7A. GenBank Reports for Accession Numbers CAA25649 and P01374 are submitted in support of this amendment. CAA25649 is the original GenBank submission for the Gray *et al.* article. Because the Gray GenBank report does not identify the lymphotoxin (LT) as LT-alpha, GenBank report P01374, which also cites the Gray *et al.* reference, is also included. Thus, this amendment introduces no new matter and is fully supported by the specification.

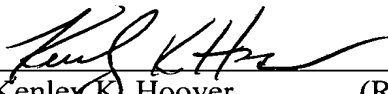
The shading of certain amino acid residues in Figure 7 indicates which amino acid residues match the consensus sequence. The amendment of the "G" at position 197 of Neutrokin-alpha sequence corrects the shading because a serine (S), and not a glycine (G) residue is the consensus residue at this position. Support for this amendment is found in Figure 2B (Formal Drawing Figure 2C) where the G at position 197 of the Neutrokin alpha polypeptide is not shaded. Thus, this amendment introduces no new matter and is fully supported by the specification.

## CONCLUSION

Applicants respectfully request that the amendments and remarks above be entered and made of record in the file history of the instant application.

Respectfully submitted,

Dated: July 28, 2000

  
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